We claim:

1. A method of detecting genetic predisposition to venous thrombosis (VT) in a subject, comprising:

determining whether the subject has one or more mutations or polymorphisms in at least eight VT-related molecules, wherein the at least eight venous thrombosis molecules comprise antithrombin III (AT III), protein C, protein S, fibrinogen, factor V (FV), prothrombin (factor II), methylenetetrahydrofolate reductase (MTHFR) and angiotensin 1-converting enzyme (ACE), and wherein the presence of one or more mutations or polymorphisms indicates that the subject has a genetic predisposition for venous thrombosis.

2. The method of claim 1, wherein the one or more mutations or polymorphisms comprise one or more mutations or polymorphisms listed in Table 1.

3. The method of claim 1, wherein the method comprises determining whether the subject has one or more mutations or polymorphisms in at least 10 of the mutations or polymorphisms listed in Table 1.

4. The method of claim 1, wherein the method comprises determining whether the subject has one or more mutations or polymorphisms in at least 50 of the mutations or polymorphisms listed in Table 1.

5. The method of claim 1, wherein the method comprises determining whether the subject has one or more mutations or polymorphisms in at least 143 of the mutations or polymorphisms listed in Table 1.

6. The method of claim 1, wherein the method comprises determining whether the subject has one or more mutations or polymorphisms in no more than 10 of the mutations or polymorphisms listed in Table 1.

7. The method of claim 2, wherein the one or more mutations or polymorphisms comprise AT III deficiency, PC deficiency, PS deficiency, fibrinogen Thr312Ala polymorphism, FV Leiden (G1691A) polymorphism, FV G1628 polymorphism, FV A4070G polymorphism, prothrombin G20210A polymorphism, MTHFR C677T and ACE intron 16, 288 bp insertion/deletion polymorphism.

8. The method of claim 1, wherein the method provides a probability of developing VT of at least 98% in Caucasians, at least 85% in Asians, and at least 87% in Africans.

9. The method of claim 1, wherein the method comprises determining whether the subject has one or more mutations or polymorphisms in at least eight VT-related molecules.

10. The method of claim 1, wherein the at least eight VT-related molecules comprise nucleic acid molecules.

11. The method of claim 10, wherein the nucleic acid molecules are amplified from the subject, thereby generating amplification products, and wherein the amplification products are hybridized with oligonucleotide probes that detect the one or more mutations or polymorphisms.

12. The method of claim 11, wherein hybridizing the oligonucleotides comprises:

incubating the amplification products with the oligonucleotide probes for a time sufficient to allow hybridization between the amplification products and oligonucleotide probes, thereby forming amplification products: oligonucleotide probe complexes; and

analyzing the amplification products: oligonucleotide probe complexes to determine if the amplification products comprise one or more mutations or polymorphisms in the VT-related nucleic acids, wherein the presence of one or more

mutations or polymorphisms indicates that the subject has a genetic predisposition for VT.

13. The method of claim 12, wherein analyzing the amplification products:oligonucleotide probe complexes comprises determining an amount of nucleic acid hybridization, and wherein a greater amount of hybridization to one or more of the mutated sequences, as compared to an amount of hybridization to a corresponding wild-type sequence, indicates that the subject has a genetic predisposition for VT.

14. The method of claim 12, wherein analyzing the amplification products:oligonucleotide probe complexes includes detecting and quantifying the complexes.

15. The method of claim 11, wherein the oligonucleotide probes are present on an array substrate.

16. The method of claim 15, wherein the array further comprises oligonucleotide probes complementary to wild-type VT-related nucleic acid molecules.

17. The method of claim 16, wherein the wild-type VT-related nucleic acid molecules comprise oligonucleotide probes complementary to wild-type AT III, wild-type protein C, wild-type protein S, wild-type fibrinogen, wild-type factor V, wild-type factor II, wild-type MTHFR and wild-type ACE nucleic acid sequences.

18. The method of claim 1, wherein the at least eight VT-related molecules consist of sequences from AT III, protein C, protein S, fibrinogen, factor V, factor II, , MTHFR and ACE.

19. The method of claim 1, wherein the subject is in a group potentially at risk of

developing a venous thrombosis.

20. The method of claim 19, wherein the subject is pregnant, is in puerperium, is using oral contraceptives or hormone replacement therapy, has previous thrombosis history, has or will undergo prolonged immobilization, has a myeloproliferative disorder, has a malignancy, has or will undergo surgery, has a bone fracture, is of advanced age, has antiphospholipid antibodies, or combinations thereof.

21. The method of claim 11, wherein the nucleic acid molecules obtained from the subject are obtained from serum.

22. A method of detecting genetic predisposition to VT in a subject, comprising:

applying amplification products to an array, wherein the array comprises oligonucleotide probes complementary to mutated AT III, mutated protein C, mutated protein S, mutated fibrinogen, mutated factor V, mutated factor II, mutated MTHFR and mutated ACE sequences, and wherein the amplification products comprise nucleic acid sequences from AT III, protein C, protein S, fibrinogen, factor V, factor II, MTHFR and ACE, obtained from the subject;

incubating the amplification products with the array for a time sufficient to allow hybridization between the amplification products and oligonucleotide probes, thereby forming amplification products: oligonucleotide probe complexes; and

analyzing the amplification products: oligonucleotide probe complexes to determine if the amplification products comprise one or more mutations or polymorphisms in the AT III, protein C, protein S, fibrinogen, factor V, factor II, MTHFR or ACE sequences, wherein the presence of one or more mutations or polymorphisms indicates that the subject has a genetic predisposition for VT.

23. A method of selecting a venous thrombosis (VT) therapy, comprising:

detecting a mutation or polymorphism in at least one VT-related molecule of a

subject, using the method of claim 1; and

if such mutation or polymorphism is identified, selecting a treatment to avoid or reduce VT, or to delay the onset of VT.

24. The method of claim 23, further comprising administering the selected treatment to the subject.

25. The method of claim 24, wherein the selected treatment comprises treating the subject with an anticoagulant agent.

26. An array comprising oligonucleotide probes complementary to wild-type gene sequences, mutated gene sequences, or both, wherein the gene sequences comprise coding or non-coding sequences from AT III, protein C, protein S, fibrinogen, factor V, factor II, MTHFR and ACE genes.

27. The array of claim 26, wherein the mutated gene sequences comprise ten or more mutations or polymorphisms listed in Table 1.

28. The array of claim 27, wherein the mutated gene sequences consist essentially of the mutations or polymorphisms listed in Table 1.

29. A method of detecting a genetic predisposition to venous thrombosis (VT) in a subject, comprising:

applying amplification products to the array of claim 13, wherein the amplification products comprise amplified nucleic acids obtained from the subject, wherein the nucleic acids comprise coding or non-coding sequences from AT III, protein C, protein S, fibrinogen, factor V, factor II, , MTHFR and ACE.

incubating the amplification products with the array for a time sufficient to allow hybridization between the amplification products and oligonucleotide probes, thereby

forming amplification products: oligonucleotide probe complexes; and

analyzing the amplification products: oligonucleotide probe complexes to determine if the amplification products comprise one or more mutations or polymorphisms in the AT III, protein C, protein S, fibrinogen, factor V, factor II, MTHFR, or ACE genes, wherein the presence of one or more mutations or polymorphisms indicates that the subject has a genetic predisposition for VT.

30. A kit for detecting a genetic predisposition to venous thrombosis (VT) in a subject, comprising:

a solid phase nucleic acid array comprising a plurality of oligonucleotide probes chemically linked to a solid polymeric support surface in a predetermined pattern, wherein the oligonucleotide probes are capable of hybridizing under stringent conditions to one or more nucleic acid molecules having VT-related mutations or polymorphisms in AT III, protein C, protein S, fibrinogen, factor V, factor II, MTHFR and ACE genes.

31. The kit of claim 30, wherein the oligonucleotides comprise SEQ ID NOS: 1-287.

32. The kit of claim 30, further comprising primers for amplifying nucleic acid molecules obtained from the subject to obtain amplification products, in separate packaging, wherein the amplification products comprise sequences from AT III, protein C, protein S, fibrinogen, factor V, factor II, MTHFR, and ACE genes;

33. The kit of claim 30, further comprising an amplification enzyme, in separate packaging.

34. The kit of claim 30, further comprising a buffer solution, in separate packaging.

35. The kit of claim 30, wherein the array further comprises oligonucleotides capable of hybridizing under stringent conditions to a wild-type AT III, wild-type protein C, wild-

type protein S, wild-type fibrinogen, wild-type factor V, wild-type factor II, wild-type MTHFR, and wild-type ACE.